

## SEQUENCE LISTING

<110> Arkray, Inc.

<120> Fructosylamine oxidase

<130> 663979

<150> JP 2002-277214

<151> 2002-09-24

<150> JP 2002-309734

<151> 2002-10-24

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 460

<212> DNA

<213> Fusarium proliferatum

<400> 1

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aaaccataaa taaatcaaaa ctttcaacaa cggatctctt ggttctggca tcgatgaaga 180

acgcagcaaa atgcgataag taatgtgaat tgcagaattc agtgaatcat cgaatctttg 240

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aacgcacatt gcgcccgcga gtattctggc gggcatgcct gttcgagcgt catttcaacc 300  
ctcaagcccc cgggtttggt gttggggatc ggcgagccct tgcggcaagc cggccccgaa 360  
atctagtggc ggtctcgctg cagcttccat tgcgtagtag taaaaccctc gcaactggta 420  
cgcgggcgcg ccaagccgtt aaacccccaa cttctgaatg 460

&lt;210&gt; 2

&lt;211&gt; 10

&lt;212&gt; PRT

<213> *Fusarium proliferatum*

&lt;400&gt; 2

Ala Arg Thr Val Ala Pro Leu Asn Lys Asp

1

5

10

&lt;210&gt; 3

&lt;211&gt; 1422

&lt;212&gt; DNA

<213> *Fusarium proliferatum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (1419)

&lt;223&gt;

&lt;400&gt; 3



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gac tgg ggc tac ctc aat ggc aac tct ggc tgg gct gat gcc ggg gag	528
Asp Trp Gly Tyr Leu Asn Gly Asn Ser Gly Trp Ala Asp Ala Gly Glu	
165 170 175	
ggt atg aag tgg ctc tat aag cag gcc cag gcc aca gga cgt att cat	576
Gly Met Lys Trp Leu Tyr Lys Gln Ala Gln Ala Thr Gly Arg Ile His	
180 185 190	
ttt gtc aac ggc aag gtg aca gag ctc gta aca gag ggt gac cga gtc	624
Phe Val Asn Gly Lys Val Thr Glu Leu Val Thr Glu Gly Asp Arg Val	
195 200 205	
att ggt gcg aaa ttg agc gat tca aag att ctc aag gcc gat gtg gtt	672
Ile Gly Ala Lys Leu Ser Asp Ser Lys Ile Leu Lys Ala Asp Val Val	
210 215 220	
atg gta gct gct ggt gct tgg tcc ggc tca ctc gtt gac ctt cga gga	720
Met Val Ala Ala Gly Ala Trp Ser Gly Ser Leu Val Asp Leu Arg Gly	
225 230 235 240	
aga aca gag gct act ggc cat gct gtc gcg tat atg gac atc aca ccg	768
Arg Thr Glu Ala Thr Gly His Ala Val Ala Tyr Met Asp Ile Thr Pro	
245 250 255	
gaa gag cag aag cga ctc gac aac ttc cct gtg gtg ttg aat ctc agc	816
Glu Glu Gln Lys Arg Leu Asp Asn Phe Pro Val Val Leu Asn Leu Ser	
260 265 270	
acc ggt ctc ttc ctc att cct cct cga aat aac gtc ctc aag gcc gcc	864
Thr Gly Leu Phe Leu Ile Pro Pro Arg Asn Asn Val Leu Lys Ala Ala	
275 280 285	
cga cac aca ttc ggg tac att aac ccg gtc aag att aac aac gct ctt	912
Arg His Thr Phe Gly Tyr Ile Asn Pro Val Lys Ile Asn Asn Ala Leu	
290 295 300	
cct cct tgc ccc aac gat aag cgg gaa cca ttc atc gca tct caa ccc	960
Pro Pro Ser Pro Asn Asp Lys Arg Glu Pro Phe Ile Ala Ser Gln Pro	
305 310 315 320	

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tac acc tct cgc aac gat tcc tca aat cct tta acc gtc gag gct gac	1008
Tyr Thr Ser Arg Asn Asp Ser Ser Asn Pro Leu Thr Val Glu Ala Asp	
325 330 335	
aaa gat ctg cgc cgc gca ctc acg gat ctg tgt cct ata cgt ggc cta	1056
Lys Asp Leu Arg Arg Ala Leu Thr Asp Leu Cys Pro Ile Arg Gly Leu	
340 345 350	
gaa acc agg cca tgg aag gag gct cga atc tgc tgg tat tcc gat aca	1104
Glu Thr Arg Pro Trp Lys Glu Ala Arg Ile Cys Trp Tyr Ser Asp Thr	
355 360 365	
cga gat ggc gag tgg ctc att gac tac cac ccg ggc tgg aag gga ctc	1152
Arg Asp Gly Glu Trp Leu Ile Asp Tyr His Pro Gly Trp Lys Gly Leu	
370 375 380	
ttt gtt gca aca ggt gac agt gga cac gga ttc aag ttc cta ccc aac	1200
Phe Val Ala Thr Gly Asp Ser Gly His Gly Phe Lys Phe Leu Pro Asn	
385 390 395 400	
ttg ggt gag aaa atc gtg gat gtt atg caa ggc cag ggt ggc aag ctt	1248
Leu Gly Glu Lys Ile Val Asp Val Met Gln Gly Gln Gly Gly Lys Leu	
405 410 415	
ggc gag aag tgg cga tgg aaa gag atc cag aat gat gga gtc gga aga	1296
Gly Glu Lys Trp Arg Trp Lys Glu Ile Gln Asn Asp Gly Val Gly Arg	
420 425 430	
gag acg aac gga gtg tac act ggt tta gtg acg gaa gat ggt agc aga	1344
Glu Thr Asn Gly Val Tyr Thr Gly Leu Val Thr Glu Asp Gly Ser Arg	
435 440 445	
ggt gga cgg ccc ttg gtg ctc tgt gat gag ctc gag aag ggc agg gcg	1392
Gly Gly Arg Pro Leu Val Leu Cys Asp Glu Leu Glu Lys Gly Arg Ala	
450 455 460	
ctt att ggg aac acc aag gcc aag cta tga	1422
Leu Ile Gly Asn Thr Lys Ala Lys Leu	
465 470	

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&lt;210&gt; 4

&lt;211&gt; 473

&lt;212&gt; PRT

<213> *Fusarium proliferatum*

&lt;400&gt; 4

Met Ala Gly Pro Pro Ser Ser Ile Leu Ile Val Gly Ser Gly Val Phe  
1 5 10 15

Gly Leu Gly Thr Ala Trp Ala Leu Ala Lys Arg Ser His Phe Ser Asn  
20 25 30

Thr Ser Ile Thr Val Val Asp Asp Cys Ala Gly Gln Phe Pro Pro Glu  
35 40 45

Asp Ala Ala Ser Val Asp Ser Ser Arg Ile Val Arg Ala Asp Tyr Ser  
50 55 60

Asp Pro Tyr Tyr Ala Ala Leu Ala Ala Glu Ala Gln Lys Glu Trp Arg  
65 70 75 80

Lys Gln Gly Asp His Glu Val Gly Gly Gln Gly Arg Tyr Ser Glu Ser  
85 90 95

Gly Phe Val Leu Cys Ala Ser Glu Thr Pro Glu Asp Phe Lys Leu Lys  
100 105 110

Lys Ser Gly Met Asp Tyr Thr Lys Glu Ser Ala Lys Asn Val Glu Leu  
115 120 125

Ile Ala Lys Glu Thr Gly Leu Pro Val Asp Lys Ile Gln Lys Leu Glu  
130 135 140

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Ser Thr Lys Ala Leu Gln Glu Phe Leu Gly Thr Asp Gly Tyr Pro Gly  
145 150 155 160

Asp Trp Gly Tyr Leu Asn Gly Asn Ser Gly Trp Ala Asp Ala Gly Glu  
165 170 175

Gly Met Lys Trp Leu Tyr Lys Gln Ala Gln Ala Thr Gly Arg Ile His  
180 185 190

Phe Val Asn Gly Lys Val Thr Glu Leu Val Thr Glu Gly Asp Arg Val  
195 200 205

Ile Gly Ala Lys Leu Ser Asp Ser Lys Ile Leu Lys Ala Asp Val Val  
210 215 220

Met Val Ala Ala Gly Ala Trp Ser Gly Ser Leu Val Asp Leu Arg Gly  
225 230 235 240

Arg Thr Glu Ala Thr Gly His Ala Val Ala Tyr Met Asp Ile Thr Pro  
245 250 255

Glu Glu Gln Lys Arg Leu Asp Asn Phe Pro Val Val Leu Asn Leu Ser  
260 265 270

Thr Gly Leu Phe Leu Ile Pro Pro Arg Asn Asn Val Leu Lys Ala Ala  
275 280 285

Arg His Thr Phe Gly Tyr Ile Asn Pro Val Lys Ile Asn Asn Ala Leu  
290 295 300

Pro Pro Ser Pro Asn Asp Lys Arg Glu Pro Phe Ile Ala Ser Gln Pro  
305 310 315 320

Tyr Thr Ser Arg Asn Asp Ser Ser Asn Pro Leu Thr Val Glu Ala Asp  
325 330 335

Lys Asp Leu Arg Arg Ala Leu Thr Asp Leu Cys Pro Ile Arg Gly Leu  
340 345 350



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Glu Thr Arg Pro Trp Lys Glu Ala Arg Ile Cys Trp Tyr Ser Asp Thr  
355 360 365

Arg Asp Gly Glu Trp Leu Ile Asp Tyr His Pro Gly Trp Lys Gly Leu  
370 375 380

Phe Val Ala Thr Gly Asp Ser Gly His Gly Phe Lys Phe Leu Pro Asn  
385 390 395 400

Leu Gly Glu Lys Ile Val Asp Val Met Gln Gly Gln Gly Gly Lys Leu  
405 410 415

Gly Glu Lys Trp Arg Trp Lys Glu Ile Gln Asn Asp Gly Val Gly Arg  
420 425 430

Glu Thr Asn Gly Val Tyr Thr Gly Leu Val Thr Glu Asp Gly Ser Arg  
435 440 445

Gly Gly Arg Pro Leu Val Leu Cys Asp Glu Leu Glu Lys Gly Arg Ala  
450 455 460

Leu Ile Gly Asn Thr Lys Ala Lys Leu  
465 470

<210> 5

<211> 1335

<212> DNA

<213> *Fusarium proliferatum*

<220>

<221> CDS

<222> (1).. (1332)

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&lt;223&gt;

&lt;400&gt; 5

atg gcc cgt act gtt gcc cgc ctc aat aag gac tca ggg att ctc atc 48  
 Met Ala Arg Thr Val Ala Pro Leu Asn Lys Asp Ser Gly Ile Leu Ile  
 1 5 10 15

gtt ggt ggc gga act tgg gga tgc tca act gcc ctc cat ctc gcc cgt 96  
 Val Gly Gly Gly Thr Trp Gly Cys Ser Thr Ala Leu His Leu Ala Arg  
 20 25 30

cgg ggt tac acc aac gtc act gtt ctc gat gtc aat cgc atc ccg tca 144  
 Arg Gly Tyr Thr Asn Val Thr Val Leu Asp Val Asn Arg Ile Pro Ser  
 35 40 45

ccg ata tca gcc ggg cat gat gta aac aaa ctt tct aac aga cta ggc 192  
 Pro Ile Ser Ala Gly His Asp Val Asn Lys Leu Ser Asn Arg Leu Gly  
 50 55 60

act tct gat agt aaa ggc gat gac gaa gac tca atc tgg aaa gct ctt 240  
 Thr Ser Asp Ser Lys Gly Asp Asp Glu Asp Ser Ile Trp Lys Ala Leu  
 65 70 75 80

acg tac gcc gca gct caa gga tgg ctc cat gat ccc atc ttc caa cct 288  
 Thr Tyr Ala Ala Ala Gln Gly Trp Leu His Asp Pro Ile Phe Gln Pro  
 85 90 95

ttc tgc cac aat aca gga gct gtc atg gct ggc tca aca cca aaa tct 336  
 Phe Cys His Asn Thr Gly Ala Val Met Ala Gly Ser Thr Pro Lys Ser  
 100 105 110

atc aag cag ctg gta gaa gat gag atc ggt gac gac atc gac cag tat 384  
 Ile Lys Gln Leu Val Glu Asp Glu Ile Gly Asp Asp Ile Asp Gln Tyr  
 115 120 125

aca cct ctc aac aca gca gaa gat ttc aga agg act atg ccg gag cgt 432  
 Thr Pro Leu Asn Thr Ala Glu Asp Phe Arg Arg Thr Met Pro Glu Arg  
 130 135 140

att ctg aca ggt gat ttt cta ggc tgg aag ggc ttt tac aag ccc aga	480
Ile Leu Thr Gly Asp Phe Leu Gly Trp Lys Gly Phe Tyr Lys Pro Arg	
145 150 155 160	
ggg tca ggt tgg gtt cat gcc aga aag gct atg aaa gct gct ttt gaa	528
Gly Ser Gly Trp Val His Ala Arg Lys Ala Met Lys Ala Ala Phe Glu	
165 170 175	
gag agc cag aga ctt ggt gtc aag ttc atc act ggc tct ccc gaa ggc	576
Glu Ser Gln Arg Leu Gly Val Lys Phe Ile Thr Gly Ser Pro Glu Gly	
180 185 190	
aag gtc gag agt ctg gtc ttt gaa gct ggt gat gtc aaa ggt gca aaa	624
Lys Val Glu Ser Leu Val Phe Glu Ala Gly Asp Val Lys Gly Ala Lys	
195 200 205	
aca gca gat gga aag gaa cac aga gcg gat cga aca att ctc tcc gct	672
Thr Ala Asp Gly Lys Glu His Arg Ala Asp Arg Thr Ile Leu Ser Ala	
210 215 220	
ggg gcc tca gca gag ttc tcc ctc gat ttt gag aac cag atc cgt cct	720
Gly Ala Ser Ala Glu Phe Ser Leu Asp Phe Glu Asn Gln Ile Arg Pro	
225 230 235 240	
acg gca tgg act ctg ggc cat atc cag atg aca gca gag gaa aca aag	768
Thr Ala Trp Thr Leu Gly His Ile Gln Met Thr Ala Glu Glu Thr Lys	
245 250 255	
ctg tac aag gaa ctt ccc ccc ctt ttc aat atc aac cag ggc ttc ttc	816
Leu Tyr Lys Glu Leu Pro Pro Leu Phe Asn Ile Asn Gln Gly Phe Phe	
260 265 270	
atg gaa ccc gat gag gac ttg cat caa ctc aag atg tgc gat gaa cat	864
Met Glu Pro Asp Glu Asp Leu His Gln Leu Lys Met Cys Asp Glu His	
275 280 285	
ccc gga tac tgc aat tgg gtt gac aaa cct ggt tcc aaa tac ccc cag	912
Pro Gly Tyr Cys Asn Trp Val Asp Lys Pro Gly Ser Lys Tyr Pro Gln	
290 295 300	

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tcc atc ccc ttc gca aag tat caa gtg cca att gag gct gaa cga cgc 960  
 Ser Ile Pro Phe Ala Lys Tyr Gln Val Pro Ile Glu Ala Glu Arg Arg  
 305 310 315 320

atg aag caa ttt ctg aaa gac atc atg cct cag ctc gca gat cgg cca 1008  
 Met Lys Gln Phe Leu Lys Asp Ile Met Pro Gln Leu Ala Asp Arg Pro  
 325 330 335

ctt gtt cat gct cga atc tgc tgg tgc gcc gat aca cag gat aga atg 1056  
 Leu Val His Ala Arg Ile Cys Trp Cys Ala Asp Thr Gln Asp Arg Met  
 340 345 350

ttt ctg atc acg tat cac cct cga cac cca tcg ctt gtc att gct tcc 1104  
 Phe Leu Ile Thr Tyr His Pro Arg His Pro Ser Leu Val Ile Ala Ser  
 355 360 365

ggg gat tgt ggc aca gga tac aag cat atc act tcc att gga aag ttc 1152  
 Gly Asp Cys Gly Thr Gly Tyr Lys His Ile Thr Ser Ile Gly Lys Phe  
 370 375 380

atc tct gat tgt atg gag ggc aca ttg gag gaa agg ttt gct aag ttc 1200  
 Ile Ser Asp Cys Met Glu Gly Thr Leu Glu Glu Arg Phe Ala Lys Phe  
 385 390 395 400

tgg aga tgg cga cca gag aag ttt acg gag ttc tgg ggt aaa gat ccc 1248  
 Trp Arg Trp Arg Pro Glu Lys Phe Thr Glu Phe Trp Gly Lys Asp Pro  
 405 410 415

ctg gat cgg ttt gga gct gac gat aag atc atg gat ttg ccc aag agt 1296  
 Leu Asp Arg Phe Gly Ala Asp Asp Lys Ile Met Asp Leu Pro Lys Ser  
 420 425 430

gat gca gag gga tgg aca gac ata cag aat gat aaa taa 1335  
 Asp Ala Glu Gly Trp Thr Asp Ile Gln Asn Asp Lys  
 435 440

&lt;210&gt; 6

&lt;211&gt; 444

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&lt;212&gt; PRT

<213> *Fusarium proliferatum*

&lt;400&gt; .6

Met Ala Arg Thr Val Ala Pro Leu Asn Lys Asp Ser Gly Ile Leu Ile  
1 5 10 15

Val Gly Gly Gly Thr Trp Gly Cys Ser Thr Ala Leu His Leu Ala Arg  
20 25 30

Arg Gly Tyr Thr Asn Val Thr Val Leu Asp Val Asn Arg Ile Pro Ser  
35 40 45

Pro Ile Ser Ala Gly His Asp Val Asn Lys Leu Ser Asn Arg Leu Gly  
50 55 60

Thr Ser Asp Ser Lys Gly Asp Asp Glu Asp Ser Ile Trp Lys Ala Leu  
65 70 75 80

Thr Tyr Ala Ala Ala Gln Gly Trp Leu His Asp Pro Ile Phe Gln Pro  
85 90 95

Phe Cys His Asn Thr Gly Ala Val Met Ala Gly Ser Thr Pro Lys Ser  
100 105 110

Ile Lys Gln Leu Val Glu Asp Glu Ile Gly Asp Asp Ile Asp Gln Tyr  
115 120 125

Thr Pro Leu Asn Thr Ala Glu Asp Phe Arg Arg Thr Met Pro Glu Arg  
130 135 140

Ile Leu Thr Gly Asp Phe Leu Gly Trp Lys Gly Phe Tyr Lys Pro Arg  
145 150 155 160

Gly Ser Gly Trp Val His Ala Arg Lys Ala Met Lys Ala Ala Phe Glu  
165 170 175

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Glu Ser Gln Arg Leu Gly Val Lys Phe Ile Thr Gly Ser Pro Glu Gly  
180 185 190

Lys Val Glu Ser Leu Val Phe Glu Ala Gly Asp Val Lys Gly Ala Lys  
195 200 205

Thr Ala Asp Gly Lys Glu His Arg Ala Asp Arg Thr Ile Leu Ser Ala  
210 215 220

Gly Ala Ser Ala Glu Phe Ser Leu Asp Phe Glu Asn Gln Ile Arg Pro  
225 230 235 240

Thr Ala Trp Thr Leu Gly His Ile Gln Met Thr Ala Glu Glu Thr Lys  
245 250 255

Leu Tyr Lys Glu Leu Pro Pro Leu Phe Asn Ile Asn Gln Gly Phe Phe  
260 265 270

Met Glu Pro Asp Glu Asp Leu His Gln Leu Lys Met Cys Asp Glu His  
275 280 285

Pro Gly Tyr Cys Asn Trp Val Asp Lys Pro Gly Ser Lys Tyr Pro Gln  
290 295 300

Ser Ile Pro Phe Ala Lys Tyr Gln Val Pro Ile Glu Ala Glu Arg Arg  
305 310 315 320

Met Lys Gln Phe Leu Lys Asp Ile Met Pro Gln Leu Ala Asp Arg Pro  
325 330 335

Leu Val His Ala Arg Ile Cys Trp Cys Ala Asp Thr Gln Asp Arg Met  
340 345 350

Phe Leu Ile Thr Tyr His Pro Arg His Pro Ser Leu Val Ile Ala Ser  
355 360 365

Gly Asp Cys Gly Thr Gly Tyr Lys His Ile Thr Ser Ile Gly Lys Phe  
370 375 380

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Ile Ser Asp Cys Met Glu Gly Thr Leu Glu Glu Arg Phe Ala Lys Phe  
385 390 395 400

Trp Arg Trp Arg Pro Glu Lys Phe Thr Glu Phe Trp Gly Lys Asp Pro  
405 410 415

Leu Asp Arg Phe Gly Ala Asp Asp Lys Ile Met Asp Leu Pro Lys Ser  
420 425 430

Asp Ala Glu Gly Trp Thr Asp Ile Gln Asn Asp Lys  
435 440

&lt;210&gt; 7

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> A peptide designed on the basis of the peptide produced by *Fusarium proliferatum*

&lt;400&gt; 7

Gly Gly Asx Thr Thr Tyr Thr Thr Cys Trp Thr Ser Gly Ala Arg Cys  
1 5 10 15

Cys Asn Arg Ala Tyr Gly Ala  
20

&lt;210&gt; 8

&lt;211&gt; 19

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&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> A peptide designed on the basis of the peptide produced by *Fusarium proliferatum*

&lt;400&gt; 8

Gly	Thr	Arg	Cys	Val	Gly	Tyr	Arg	Tyr	Met	Cys	Cys	Ala	Gly	Cys	Ala
1				5					10					15	

Val Ala Thr